

SEQUENCE LISTING

<110> Brenner, Michael B.
Valencia, Xavier

<120> Methods and Compositions for Treatment
of Inflammatory Disease Using Cadherin-11 Modulating Agents

<130> B0801/7187/ERP/MAT

<150> US 60/152,456

<151> 1999-09-03

<150> US 60/153,490

<151> 1999-09-13

<160> 12

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<211> 2625

<212> DNA

<213> Homo Sapiens

<220>

<221> CDS

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agctgcattc tctgtgcctt accacgtaac caaaa atg aag gag aac tac tgt	173
Met Lys Glu Asn Tyr Cys	
1 5	

tta caa gcc gcc ctg gtg tgc ctg ggc atg ctg tgc cac agc cat gcc	221
Leu Gln Ala Ala Leu Val Cys Leu Gly Met Leu Cys His Ser His Ala	
10 15 20	

ttt gcc cca gag cgg cgg ggg cac ctg cgg ccc tcc ttc cat ggg cac	269
Phe Ala Pro Glu Arg Arg Gly His Leu Arg Pro Ser Phe His Gly His	
25 30 35	

cat gag aag ggc aag gag ggg cag gtg cta cag cgc tcc aag cgt ggc	317
His Glu Lys Gly Lys Glu Gly Gln Val Leu Gln Arg Ser Lys Arg Gly	
40 45 50	

tgg gtc tgg aac cag ttc ttc gtg ata gag gag tac acc ggg cct gac	365
Trp Val Trp Asn Gln Phe Phe Val Ile Glu Glu Tyr Thr Gly Pro Asp	
55 60 65 70	

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ccc gtg ctt gtg ggc agg ctt cat tca gat att gac tct ggt gat ggg	413
Pro Val Leu Val Gly Arg Leu His Ser Asp Ile Asp Ser Gly Asp Gly	
75 80 85	
aac att aaa tac att ctc tca ggg gaa gga gct gga acc att ttt gtg	461
Asn Ile Lys Tyr Ile Leu Ser Gly Glu Gly Ala Gly Thr Ile Phe Val	
90 95 100	
att gat gac aaa tca ggg aac att cat gcc acc aag acg ttg gat cga	509
Ile Asp Asp Lys Ser Gly Asn Ile His Ala Thr Lys Thr Leu Asp Arg	
105 110 115	
gaa gag aga gcc cag tac acg ttg atg gct cag gcg gtg gac agg gac	557
Glu Glu Arg Ala Gln Tyr Thr Leu Met Ala Gln Ala Val Asp Arg Asp	
120 125 130	
acc aat cgg cca ctg gag cca ccg tcg gaa ttc att gtc aag gtc cag	605
Thr Asn Arg Pro Leu Glu Pro Pro Ser Glu Phe Ile Val Lys Val Gln	
135 140 145 150	
gac att aat gac aac cct ccg gag ttc ctg cac gag acc tat cat gcc	653
Asp Ile Asn Asp Asn Pro Pro Glu Phe Leu His Glu Thr Tyr His Ala	
155 160 165	
aac gtg cct gag agg tcc aat gtg gga acg tca gta atc cag gtg aca	701
Asn Val Pro Glu Arg Ser Asn Val Gly Thr Ser Val Ile Gln Val Thr	
170 175 180	
gct tca gat gca gat gac ccc act tat gga aat agc gcc aag tta gtg	749
Ala Ser Asp Ala Asp Asp Pro Thr Tyr Gly Asn Ser Ala Lys Leu Val	
185 190 195	
tac agt atc ctc gaa gga caa ccc tat ttt tcg gtg gaa gca cag aca	797
Tyr Ser Ile Leu Glu Gly Gln Pro Tyr Phe Ser Val Glu Ala Gln Thr	
200 205 210	
ggt atc atc aga aca gcc cta ccc aac atg gac agg gag gcc aag gag	845
Gly Ile Ile Arg Thr Ala Leu Pro Asn Met Asp Arg Glu Ala Lys Glu	
215 220 225 230	
gag tac cac gtg gtg atc cag gcc aag gac atg ggt gga cat atg ggc	893
Glu Tyr His Val Val Ile Gln Ala Lys Asp Met Gly Gly His Met Gly	
235 240 245	
gga ctc tca ggg aca acc aaa gtg acg atc aca ctg acc gat gtc aat	941
Gly Leu Ser Gly Thr Thr Lys Val Thr Ile Thr Leu Thr Asp Val Asn	
250 255 260	
gac aac cca cca aag ttt ccg cag agg cta tac cag atg tct gtg tca	989
Asp Asn Pro Pro Lys Phe Pro Gln Arg Leu Tyr Gln Met Ser Val Ser	
265 270 275	
gaa gca gcc gtc cct ggg gag gaa gta gga aga gtg aaa gct aaa gat	1037
Glu Ala Ala Val Pro Gly Glu Glu Val Gly Arg Val Lys Ala Lys Asp	
280 285 290	
cca gac att gga gaa aat ggc tta gtc aca tac aat att gtt gat gga	1085
Pro Asp Ile Gly Glu Asn Gly Leu Val Thr Tyr Asn Ile Val Asp Gly	

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Asp Gly Met Glu Ser Phe Glu Ile Thr Thr Asp Tyr Glu Thr Gln Glu				
	315	320	325	
ggg gtg ata aag ctg aaa aag cct gta gat ttt gaa acc gaa aga gcc				1181
Gly Val Ile Lys Leu Lys Lys Pro Val Asp Phe Glu Thr Glu Arg Ala				
	330	335	340	
tat agc ttg aag gta gag gca gcc aac gtg cac atc gac ccg aag ttt				1229
Tyr Ser Leu Lys Val Glu Ala Ala Asn Val His Ile Asp Pro Lys Phe				
	345	350	355	
atc agc aat ggc cct ttc aag gac act gtg acc gtc aag atc tca gta				1277
Ile Ser Asn Gly Pro Phe Lys Asp Thr Val Thr Val Lys Ile Ser Val				
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gaa gat gct gat gag ccc cct atg ttc ttg gcc cca agt tac atc cac				1325
Glu Asp Ala Asp Glu Pro Pro Met Phe Leu Ala Pro Ser Tyr Ile His				
	375	380	385	390
gaa gtc caa gaa aat gca gct gct ggc acc gtg gtt ggg aga gtg cat				1373
Glu Val Gln Glu Asn Ala Ala Ala Gly Thr Val Val Gly Arg Val His				
	395	400	405	
gcc aaa gac cct gat gct gcc aac agc ccg ata agg tat tcc atc gat				1421
Ala Lys Asp Pro Asp Ala Ala Asn Ser Pro Ile Arg Tyr Ser Ile Asp				
	410	415	420	
cgt cac act gac ctc gac aga ttt ttc act att aat cca gag gat ggt				1469
Arg His Thr Asp Leu Asp Arg Phe Phe Thr Ile Asn Pro Glu Asp Gly				
	425	430	435	
ttt att aaa act aca aaa cct ctg gat aga gag gaa aca gcc tgg ctc				1517
Phe Ile Lys Thr Thr Lys Pro Leu Asp Arg Glu Glu Thr Ala Trp Leu				
	440	445	450	
aac atc act gtc ttt gca gca gaa atc cac aat cgg cat cag gaa gcc				1565
Asn Ile Thr Val Phe Ala Ala Glu Ile His Asn Arg His Gln Glu Ala				
	455	460	465	470
caa gtc cca gtg gcc att agg gtc ctt gat gtc aac gat aat gct ccc				1613
Gln Val Pro Val Ala Ile Arg Val Leu Asp Val Asn Asp Asn Ala Pro				
	475	480	485	
aag ttt gct gcc cct tat gaa ggt ttc atc tgt gag agt gat cag acc				1661
Lys Phe Ala Ala Pro Tyr Glu Gly Phe Ile Cys Glu Ser Asp Gln Thr				
	490	495	500	
aag cca ctt tcc aac cag cca att gtt aca att agt gca gat gac aag				1709
Lys Pro Leu Ser Asn Gln Pro Ile Val Thr Ile Ser Ala Asp Asp Lys				
	505	510	515	
gat gac acg gcc aat gga cca aga ttt atc ttc agc cta ccc cct gaa				1757
Asp Asp Thr Ala Asn Gly Pro Arg Phe Ile Phe Ser Leu Pro Pro Glu				
	520	525	530	

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Ile Ile His Asn Pro Asn Phe Thr Val Arg Asp Asn Arg Asp Asn Thr	
535 540 545 550	
gca ggc gtg tac gcc cgg cgt gga ggg ttc agt cgg cag aag cag gac	1853
Ala Gly Val Tyr Ala Arg Arg Gly Gly Phe Ser Arg Gln Lys Gln Asp	
555 560 565	
ttg tac ctt ctg ccc ata gtg atc agc gat ggc ggc atc ccg ccc atg	1901
Leu Tyr Leu Leu Pro Ile Val Ile Ser Asp Gly Gly Ile Pro Pro Met	
570 575 580	
agt agc acc aac acc ctc acc atc aaa gtc tgc ggg tgc gac gtg aac	1949
Ser Ser Thr Asn Thr Leu Thr Ile Lys Val Cys Gly Cys Asp Val Asn	
585 590 595	
ggg gca ctg ctc tcc tgc aac gca gag gcc tac att ctg aac gcc ggc	1997
Gly Ala Leu Leu Ser Cys Asn Ala Glu Ala Tyr Ile Leu Asn Ala Gly	
600 605 610	
ctg agc aca ggc gcc ctg atc gcc atc ctc gcc tgc atc gtc att ctc	2045
Leu Ser Thr Gly Ala Leu Ile Ala Ile Leu Ala Cys Ile Val Ile Leu	
615 620 625 630	
ctg gtc att gta gta ttg ttt gtg acc ctg aga agg caa aag aaa gaa	2093
Leu Val Ile Val Val Leu Phe Val Thr Leu Arg Arg Gln Lys Lys Glu	
635 640 645	
cca ctc att gtc ttt gag gaa gaa gat gtc cgt gag aac atc att act	2141
Pro Leu Ile Val Phe Glu Glu Glu Asp Val Arg Glu Asn Ile Ile Thr	
650 655 660	
tat gat gat gaa ggg ggt ggg gaa gaa gac aca gaa gcc ttt gat att	2189
Tyr Asp Asp Glu Gly Gly Gly Glu Glu Asp Thr Glu Ala Phe Asp Ile	
665 670 675	
gcc acc ctc cag aat cct gat ggt atc aat gga ttt atc ccc cgc aaa	2237
Ala Thr Leu Gln Asn Pro Asp Gly Ile Asn Gly Phe Ile Pro Arg Lys	
680 685 690	
gac atc aaa cct gag tat cag tac atg cct aga cct ggg ctc cgg cca	2285
Asp Ile Lys Pro Glu Tyr Gln Tyr Met Pro Arg Pro Gly Leu Arg Pro	
695 700 705 710	
gcg ccc aac agc gtg gat gtc gat gac ttc atc aac acg aga ata cag	2333
Ala Pro Asn Ser Val Asp Val Asp Asp Phe Ile Asn Thr Arg Ile Gln	
715 720 725	
gag gca gac aat gac ccc acg gct cct cct tat gac tcc att caa atc	2381
Glu Ala Asp Asn Asp Pro Thr Ala Pro Pro Tyr Asp Ser Ile Gln Ile	
730 735 740	
tac ggt tat gaa ggc agg ggc tca gtg gcc ggg tcc ctg agc tcc cta	2429
Tyr Gly Tyr Glu Gly Arg Gly Ser Val Ala Gly Ser Leu Ser Ser Leu	
745 750 755	
gag tgc gcc acc aca gat tca gac ttg gac tat gat tat cta cag aac	2477
Glu Ser Ala Thr Thr Asp Ser Asp Leu Asp Tyr Asp Tyr Leu Gln Asn	

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765

770

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Trp Gly Pro Arg Phe Lys Lys Leu Ala Asp Leu Tyr Gly Ser Lys Asp
775 780 785 790

act ttt gat gac gat tct taa caataacgat acaaatttgg ccttaagaac 2576
Thr Phe Asp Asp Asp Ser *
795

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Pro	Ser	Phe	His	Gly	His	His	Glu	Lys	Gly	Lys	Glu	Gly	Gln	Val	Leu
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Glu	Tyr	Thr	Gly	Pro	Asp	Pro	Val	Leu	Val	Gly	Arg	Leu	His	Ser	Asp
65					70					75				80	
Ile	Asp	Ser	Gly	Asp	Gly	Asn	Ile	Lys	Tyr	Ile	Leu	Ser	Gly	Glu	Gly
				85					90					95	
Ala	Gly	Thr	Ile	Phe	Val	Ile	Asp	Asp	Lys	Ser	Gly	Asn	Ile	His	Ala
			100					105					110		
Thr	Lys	Thr	Leu	Asp	Arg	Glu	Glu	Arg	Ala	Gln	Tyr	Thr	Leu	Met	Ala
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Gln	Ala	Val	Asp	Arg	Asp	Thr	Asn	Arg	Pro	Leu	Glu	Pro	Pro	Ser	Glu
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Phe	Ile	Val	Lys	Val	Gln	Asp	Ile	Asn	Asp	Asn	Pro	Pro	Glu	Phe	Leu
145					150					155					160
His	Glu	Thr	Tyr	His	Ala	Asn	Val	Pro	Glu	Arg	Ser	Asn	Val	Gly	Thr
				165					170					175	
Ser	Val	Ile	Gln	Val	Thr	Ala	Ser	Asp	Ala	Asp	Asp	Pro	Thr	Tyr	Gly
			180					185					190		
Asn	Ser	Ala	Lys	Leu	Val	Tyr	Ser	Ile	Leu	Glu	Gly	Gln	Pro	Tyr	Phe
		195					200					205			
Ser	Val	Glu	Ala	Gln	Thr	Gly	Ile	Ile	Arg	Thr	Ala	Leu	Pro	Asn	Met
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Asp	Arg	Glu	Ala	Lys	Glu	Glu	Tyr	His	Val	Val	Ile	Gln	Ala	Lys	Asp
225					230					235				240	
Met	Gly	Gly	His	Met	Gly	Gly	Leu	Ser	Gly	Thr	Thr	Lys	Val	Thr	Ile
				245					250					255	
Thr	Leu	Thr	Asp	Val	Asn	Asp	Asn	Pro	Pro	Lys	Phe	Pro	Gln	Arg	Leu
			260				265						270		
Tyr	Gln	Met	Ser	Val	Ser	Glu	Ala	Ala	Val	Pro	Gly	Glu	Glu	Val	Gly
		275					280					285			
Arg	Val	Lys	Ala	Lys	Asp	Pro	Asp	Ile	Gly	Glu	Asn	Gly	Leu	Val	Thr
	290					295					300				
Tyr	Asn	Ile	Val	Asp	Gly	Asp	Gly	Met	Glu	Ser	Phe	Glu	Ile	Thr	Thr
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785 790 795

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22

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31

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23

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<400> 12
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32

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